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Current experiment and analysis paradigm in biomedical and biological research is to reduce heterogeneity in the data to ensure the conclusions are not confounded by biological, technological and demographic factors. However, this paradigm does not account for the real-world patient population heterogeneity, which in turn requires replication in multiple independent cohorts prior to translation into clinical practice. Consequently, biomedical research today is slow, expensive, and experiencing reproducibility crisis because a homogeneous cohort does not represent the real-world biological heterogeneity. I will describe an *in silico* analytic framework that turns the current paradigm on its head. This talk will focus on how heterogeneity across independent experiments can lead to identification of disease signatures that are diagnostic, prognostic, therapeutic and mechanistic across a broad spectrum of diseases including infections, autoimmune diseases, cancer, organ transplant, and vaccination. I will also discuss how biological and technical heterogeneity in publicly-available data can be leveraged to make translational medicine better, faster, cheaper, and more generalizable.

Wednesday, May 6, 2020
4 p.m. to 5 p.m. Webinar

Hosted by Steven Kleinstein, PhD and Naftali Kaminski, MD